N. Davis

1642

```
RAW SEQUENCE LISTING              DATE: 08/02/2001
PATENT APPLICATION:  US/09/536,087    TIME: 17:30:24

     Input Set : A:\10287-051001.txt
     Output Set: N:\CRF3\08022001\I536087.raw

 4 <110> APPLICANT: Detmar, Michael J.
 5        Streit, Michael
 7 <120> TITLE OF INVENTION: THROMBOSPONDIN-2 AND USES THEREOF
 9 <130> FILE REFERENCE: 10287-051001
11 <140> CURRENT APPLICATION NUMBER: 09/536,087
12 <141> CURRENT FILING DATE: 2000-03-24
14 <150> PRIOR APPLICATION NUMBER: 60/127,221
15 <151> PRIOR FILING DATE: 1999-03-31
17 <160> NUMBER OF SEQ ID NOS: 11
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3596
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (26)...(3541)
30 <400> SEQUENCE: 1
31 caggagctca gctgcaggag gcagg atg gtc tgg agg ctg gtc ctg ctg gct    52
32                            Met Val Trp Arg Leu Val Leu Leu Ala
33                            1               5
35 ctg tgg gtg tgg ccc agc acg caa gct ggt cac cag gac aaa gac acg   100
36 Leu Trp Val Trp Pro Ser Thr Gln Ala Gly His Gln Asp Lys Asp Thr
37 10                 15                  20                  25
39 acc ttc gac ctt ttc agt atc agc aac atc aac cgc aag acc att ggc   148
40 Thr Phe Asp Leu Phe Ser Ile Ser Asn Ile Asn Arg Lys Thr Ile Gly
41                 30                  35                  40
43 gcc aag cag ttc cgc ggg ccc gac ccc ggc gtg ccg gct tac cgc ttc   196
44 Ala Lys Gln Phe Arg Gly Pro Asp Pro Gly Val Pro Ala Tyr Arg Phe
45              45                  50                  55
47 gtg cgc ttt gac tac atc cca ccg gtg aac gca gat gac ctc agc aag   244
48 Val Arg Phe Asp Tyr Ile Pro Pro Val Asn Ala Asp Asp Leu Ser Lys
49           60                  65                  70
51 atc acc aag atc atg cgg cag aag gag ggc ttc ttc ctc acg gcc cag   292
52 Ile Thr Lys Ile Met Arg Gln Lys Glu Gly Phe Phe Leu Thr Ala Gln
53        75                  80                  85
55 ctc aag cag gac ggc aag tcc agg ggc acg ctg ttg gct ctg gag ggc   340
56 Leu Lys Gln Asp Gly Lys Ser Arg Gly Thr Leu Leu Ala Leu Glu Gly
57 90                  95                  100                 105
59 ccc ggt ctc tcc cag agg cag ttc gag atc gtc tcc aat ggc ccc gcg   388
60 Pro Gly Leu Ser Gln Arg Gln Phe Glu Ile Val Ser Asn Gly Pro Ala
61                 110                 115                 120
63 gac acg ctg gat ctc acc tac tgg att gac ggc acc cgg cat gtg gtc   436
64 Asp Thr Leu Asp Leu Thr Tyr Trp Ile Asp Gly Thr Arg His Val Val
65                 125                 130                 135
67 tcc ctg gag gac gtc ggc ctg gct gac tcg cag tgg aag aac gtc acc   484
68 Ser Leu Glu Asp Val Gly Leu Ala Asp Ser Gln Trp Lys Asn Val Thr
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69          140                   145                   150
71 gtg cag gtg gct ggc gag acc tac agc ttg cac gtg ggc tgc gac ctc      532
72 Val Gln Val Ala Gly Glu Thr Tyr Ser Leu His Val Gly Cys Asp Leu
73      155                   160                   165
75 ata gac agc ttc gct ctg gac gag ccc ttc tac gag cac ctg cag gcg      580
76 Ile Asp Ser Phe Ala Leu Asp Glu Pro Phe Tyr Glu His Leu Gln Ala
77 170                   175                   180                   185
79 gaa aag agc cgg atg tac gtg gcc aaa ggc tct gcc aga gag agt cac      628
80 Glu Lys Ser Arg Met Tyr Val Ala Lys Gly Ser Ala Arg Glu Ser His
81                   190                   195                   200
83 ttc agg ggt ttg ctt cag aac gtc cac cta gtg ttt gaa aac tct gtg      676
84 Phe Arg Gly Leu Leu Gln Asn Val His Leu Val Phe Glu Asn Ser Val
85                   205                   210                   215
87 gaa gat att cta agc aag aag ggt tgc cag caa ggc cag gga gct gag      724
88 Glu Asp Ile Leu Ser Lys Lys Gly Cys Gln Gln Gly Gln Gly Ala Glu
89          220                   225                   230
91 atc aac gcc atc agt gag aac aca gag acg ctg cgc ctg ggt ccg cat      772
92 Ile Asn Ala Ile Ser Glu Asn Thr Glu Thr Leu Arg Leu Gly Pro His
93      235                   240                   245
95 gtc acc acc gag tac gtg ggc ccc agc tca gag agg agg ccc gag gtg      820
96 Val Thr Thr Glu Tyr Val Gly Pro Ser Ser Glu Arg Arg Pro Glu Val
97 250                   255                   260                   265
99 tgc gaa cgc tcg tgc gag gag ctg gga aac atg gtc cag gag ctc tcg      868
100 Cys Glu Arg Ser Cys Glu Glu Leu Gly Asn Met Val Gln Glu Leu Ser
101                  270                   275                   280
103 ggg ctc cac gtc ctc gtg aac cag ccc agc gag aac ctc aag aga gtg     916
104 Gly Leu His Val Leu Val Asn Gln Pro Ser Glu Asn Leu Lys Arg Val
105                  285                   290                   295
107 tcg aat gat aac cag ttt ctc tgg gag ctc att ggt ggc cct cct aag     964
108 Ser Asn Asp Asn Gln Phe Leu Trp Glu Leu Ile Gly Gly Pro Pro Lys
109          300                   305                   310
111 aca agg aac atg tca gct tgc tgg cag gat ggc cgg ttc ttt gcg gaa     1012
112 Thr Arg Asn Met Ser Ala Cys Trp Gln Asp Gly Arg Phe Phe Ala Glu
113      315                   320                   325
115 aat gaa acg tgg gtg gtg gac agc tgc acc acg tgt acc tgc aag aaa     1060
116 Asn Glu Thr Trp Val Val Asp Ser Cys Thr Thr Cys Thr Cys Lys Lys
117 330                  335                   340                   345
119 ttt aaa acc att tgc cac caa atc acc tgc ccg cct gca acc tgc gcc     1108
120 Phe Lys Thr Ile Cys His Gln Ile Thr Cys Pro Pro Ala Thr Cys Ala
121                  350                   355                   360
123 agt cca tcc ttt gtg gaa ggc gaa tgc tgc cct tcc tgc ctc cac tcg     1156
124 Ser Pro Ser Phe Val Glu Gly Glu Cys Cys Pro Ser Cys Leu His Ser
125          365                   370                   375
127 gtg gac ggt gag gag ggc tgg tct ccg tgg gca gag tgg acc cag tgc     1204
128 Val Asp Gly Glu Glu Gly Trp Ser Pro Trp Ala Glu Trp Thr Gln Cys
129          380                   385                   390
131 tcc gtg acg tgt ggc tct ggg acc cag cag aga ggc cgg tcc tgt gac     1252
132 Ser Val Thr Cys Gly Ser Gly Thr Gln Gln Arg Gly Arg Ser Cys Asp
133      395                   400                   405
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135 gtc acc agc aac acc tgc ttg ggg ccc tcc atc cag aca cgg gct tgc        1300
136 Val Thr Ser Asn Thr Cys Leu Gly Pro Ser Ile Gln Thr Arg Ala Cys
137 410               415               420               425
139 agt ctg agc aag tgt gac acc cgc atc cgg cag gac ggc ggc tgg agc        1348
140 Ser Leu Ser Lys Cys Asp Thr Arg Ile Arg Gln Asp Gly Gly Trp Ser
141               430               435               440
143 cac tgg tca cct tgg tct tca tgc tct gtg acc tgt gga gtt ggc aat        1396
144 His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr Cys Gly Val Gly Asn
145               445               450               455
147 atc aca cgc atc cgt ctc tgc aac tcc cca gtg ccc cag atg ggg ggc        1444
148 Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Val Pro Gln Met Gly Gly
149          460               465               470
151 aag aat tgc aaa ggg agt ggc cgg gag acc aaa gcc tgc cag ggc gcc        1492
152 Lys Asn Cys Lys Gly Ser Gly Arg Glu Thr Lys Ala Cys Gln Gly Ala
153       475               480               485
155 cca tgc cca atc gat ggc cgc tgg agc ccc tgg tcc ccg tgg tcg gcc        1540
156 Pro Cys Pro Ile Asp Gly Arg Trp Ser Pro Trp Ser Pro Trp Ser Ala
157 490               495               500               505
159 tgc act gtc acc tgt gcc ggt ggg atc cgg gag cgc acc cgg gtc tgc        1588
160 Cys Thr Val Thr Cys Ala Gly Gly Ile Arg Glu Arg Thr Arg Val Cys
161               510               515               520
163 aac agc cct gag cct cag tac gga ggg aag gcc tgc gtg ggg gat gtg        1636
164 Asn Ser Pro Glu Pro Gln Tyr Gly Gly Lys Ala Cys Val Gly Asp Val
165               525               530               535
167 cag gag cgt cag atg tgc aac aag agg agc tgc ccc gtg gat ggc tgt        1684
168 Gln Glu Arg Gln Met Cys Asn Lys Arg Ser Cys Pro Val Asp Gly Cys
169          540               545               550
171 tta tcc aac ccc tgc ttc ccg gga gcc cag tgc agc agc ttc ccc gat        1732
172 Leu Ser Asn Pro Cys Phe Pro Gly Ala Gln Cys Ser Ser Phe Pro Asp
173       555               560               565
175 ggg tcc tgg tca tgc ggc tcc tgc cct gtg ggc ttc ttg ggc aat ggc        1780
176 Gly Ser Trp Ser Cys Gly Ser Cys Pro Val Gly Phe Leu Gly Asn Gly
177 570               575               580               585
179 acc cac tgt gag gac ctg gac gag tgt gcc ctg gtc ccc gac atc tgc        1828
180 Thr His Cys Glu Asp Leu Asp Glu Cys Ala Leu Val Pro Asp Ile Cys
181               590               595               600
183 ttc tcc acc agc aag gtg cct cgc tgt gtc aac act cag cct ggc ttc        1876
184 Phe Ser Thr Ser Lys Val Pro Arg Cys Val Asn Thr Gln Pro Gly Phe
185               605               610               615
187 cac tgc ctg ccc tgc ccg ccc cga tac aga ggg aac cag ccc gtc ggg        1924
188 His Cys Leu Pro Cys Pro Pro Arg Tyr Arg Gly Asn Gln Pro Val Gly
189          620               625               630
191 gtc ggc ctg gaa gca gcc aag acg gaa aag caa gtg tgt gag ccc gaa        1972
192 Val Gly Leu Glu Ala Ala Lys Thr Glu Lys Gln Val Cys Glu Pro Glu
193       635               640               645
195 aac cca tgc aag gac aag aca cac aac tgc cac aag cac gcg gag tgc        2020
196 Asn Pro Cys Lys Asp Lys Thr His Asn Cys His Lys His Ala Glu Cys
197 650               655               660               665
199 atc tac ctg ggc cac ttc agc gac ccc atg tac aag tgc gag tgc cag        2068
```

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200 Ile Tyr Leu Gly His Phe Ser Asp Pro Met Tyr Lys Cys Glu Cys Gln
201             670             675             680
203 aca ggc tac gcg ggc gac ggg ctc atc tgc ggg gag gac tcg gac ctg      2116
204 Thr Gly Tyr Ala Gly Asp Gly Leu Ile Cys Gly Glu Asp Ser Asp Leu
205             685             690             695
207 gac ggc tgg ccc aac ctc aat ctg gtc tgc gcc acc aac gcc acc tac      2164
208 Asp Gly Trp Pro Asn Leu Asn Leu Val Cys Ala Thr Asn Ala Thr Tyr
209             700             705             710
211 cac tgc atc aag gat aac tgc ccc cat ctg cca aat tct ggg cag gaa      2212
212 His Cys Ile Lys Asp Asn Cys Pro His Leu Pro Asn Ser Gly Gln Glu
213     715                     720             725
215 gac ttt gac aag gac ggg att ggc gat gcc tgt gat gat gac gat gac      2260
216 Asp Phe Asp Lys Asp Gly Ile Gly Asp Ala Cys Asp Asp Asp Asp Asp
217 730                     735             740                 745
219 aat gac ggt gtg acc gat gag aag gac aac tgc cag ctc ctc ttc aat      2308
220 Asn Asp Gly Val Thr Asp Glu Lys Asp Asn Cys Gln Leu Leu Phe Asn
221             750             755             760
223 ccc cgc cag gct gac tat gac aag gat gag gtt ggg gac cgc tgt gac      2356
224 Pro Arg Gln Ala Asp Tyr Asp Lys Asp Glu Val Gly Asp Arg Cys Asp
225             765             770             775
227 aac tgc cct tac gtg cac aac cct gcc cag atc gac aca gac aac aat      2404
228 Asn Cys Pro Tyr Val His Asn Pro Ala Gln Ile Asp Thr Asp Asn Asn
229             780             785             790
231 gga gag ggt gac gcc tgc tcc gtg gac att gat ggg gac gat gtc ttc      2452
232 Gly Glu Gly Asp Ala Cys Ser Val Asp Ile Asp Gly Asp Asp Val Phe
233     795                 800             805
235 aat gaa cga gac aat tgt ccc tac gtc tac aac act gac cag agg gac      2500
236 Asn Glu Arg Asp Asn Cys Pro Tyr Val Tyr Asn Thr Asp Gln Arg Asp
237 810                     815             820                 825
239 acg gat ggt gac ggt gtg ggg gat cac tgt gac aac tgc ccc ctg gtg      2548
240 Thr Asp Gly Asp Gly Val Gly Asp His Cys Asp Asn Cys Pro Leu Val
241             830             835             840
243 cac aac cct gac cag acc gac gtg gac aat gac ctt gtt ggg gac cag      2596
244 His Asn Pro Asp Gln Thr Asp Val Asp Asn Asp Leu Val Gly Asp Gln
245             845             850             855
247 tgt gac aac aac gag gac ata gat gac gac ggc cac cag aac aac cag      2644
248 Cys Asp Asn Asn Glu Asp Ile Asp Asp Asp Gly His Gln Asn Asn Gln
249             860             865             870
251 gac aac tgc ccc tac atc tcc aac gcc aac cag gct gac cat gac aga      2692
252 Asp Asn Cys Pro Tyr Ile Ser Asn Ala Asn Gln Ala Asp His Asp Arg
253     875                 880             885
255 gac ggc cag ggc gac gcc tgt gac cct gat gat gac aac gat ggc gtc      2740
256 Asp Gly Gln Gly Asp Ala Cys Asp Pro Asp Asp Asp Asn Asp Gly Val
257 890                 895             900                 905
259 ccc gat gac agg gac aac tgc cgg ctt gtg ttc aac cca gac cag gag      2788
260 Pro Asp Asp Arg Asp Asn Cys Arg Leu Val Phe Asn Pro Asp Gln Glu
261             910             915             920
263 gac ttg gac ggt gat gga cgg ggt gat att tgt aaa gat gat ttt gac      2836
264 Asp Leu Asp Gly Asp Gly Arg Gly Asp Ile Cys Lys Asp Asp Phe Asp
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PATENT APPLICATION: US/09/536,087   TIME: 17:30:24

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```
265                925                930                935
267 aat gac aac atc cca gat att gat gat gtg tgt cct gaa aac aat gcc    2884
268 Asn Asp Asn Ile Pro Asp Ile Asp Asp Val Cys Pro Glu Asn Asn Ala
269         940                945                950
271 atc agt gag aca gac ttc agg aac ttc cag atg gtc ccc ttg gat ccc    2932
272 Ile Ser Glu Thr Asp Phe Arg Asn Phe Gln Met Val Pro Leu Asp Pro
273     955                960                965
275 aaa ggg acc acc caa att gat ccc aac tgg gtc att cgc cat caa ggc    2980
276 Lys Gly Thr Thr Gln Ile Asp Pro Asn Trp Val Ile Arg His Gln Gly
277 970                975                980                985
279 aag gag ctg gtt cag aca gcc aac tcg gac ccc ggc atc gct gta ggt    3028
280 Lys Glu Leu Val Gln Thr Ala Asn Ser Asp Pro Gly Ile Ala Val Gly
281                990                995                1000
283 ttt gac gag ttt ggg tct gtg gac ttc agt ggc aca ttc tac gta aac    3076
284 Phe Asp Glu Phe Gly Ser Val Asp Phe Ser Gly Thr Phe Tyr Val Asn
285             1005                1010                1015
287 act gac cgg gac gac gac tat gcc ggc ttc gtc ttt ggt tac cag tca    3124
288 Thr Asp Arg Asp Asp Asp Tyr Ala Gly Phe Val Phe Gly Tyr Gln Ser
289         1020                1025                1030
291 agc agc cgc ttc tat gtg gtg atg tgg aag cag gtg acg cag acc tac    3172
292 Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln Val Thr Gln Thr Tyr
293     1035                1040                1045
295 tgg gag gac cag ccc acg cgg gcc tat ggc tac tcc ggc gtg tcc ctc    3220
296 Trp Glu Asp Gln Pro Thr Arg Ala Tyr Gly Tyr Ser Gly Val Ser Leu
297 1050                1055                1060                1065
299 aag gtg gtg aac tcc acc acg ggg acg ggc gag cac ctg agg aac gcg    3268
300 Lys Val Val Asn Ser Thr Thr Gly Thr Gly Glu His Leu Arg Asn Ala
301                1070                1075                1080
303 ctg tgg cac acg ggg aac acg ccg ggg cag gtg cga acc tta tgg cac    3316
304 Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val Arg Thr Leu Trp His
305             1085                1090                1095
307 gac ccc agg aac att ggc tgg aag gac tac acg gcc tat agg tgg cac    3364
308 Asp Pro Arg Asn Ile Gly Trp Lys Asp Tyr Thr Ala Tyr Arg Trp His
309         1100                1105                1110
311 ctg act cac agg ccc aag acc ggc tac atc aga gtc tta gtg cat gaa    3412
312 Leu Thr His Arg Pro Lys Thr Gly Tyr Ile Arg Val Leu Val His Glu
313     1115                1120                1125
315 gga aaa cag gtc atg gca gac tca gga cct atc tat gac caa acc tac    3460
316 Gly Lys Gln Val Met Ala Asp Ser Gly Pro Ile Tyr Asp Gln Thr Tyr
317 1130                1135                1140                1145
319 gct ggc ggg cgg ctg ggt cta ttt gtc ttc tct caa gaa atg gtc tat    3508
320 Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser Gln Glu Met Val Tyr
321                1150                1155                1160
323 ttc tca gac ctc aag tac gaa tgc aga gat att taaacaagat ttgctgcatt   3561
324 Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Ile
325             1165                1170
327 tccggcaatg ccctgtgcat gccatggtcc ctaga                               3596
329 <210> SEQ ID NO: 2
330 <211> LENGTH: 1172
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VERIFICATION SUMMARY   DATE: 08/02/2001
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